Supplementary Table 1. Proportion of GABAergic interneurons (PV or NOS) or cholinergic (ChAT) interneurons coexpressing c-Fos in the nAcc mShell of VGluT2-ChR2-eYFP or VGluT2-eYFP mice after photostimulation of the VTA VGluT2-inputs.

	VGluT2-ChR2-eYFP			VGluT2-eYFP		
	Total counted neurons	c-Fos positive neurons	Mean ± sem %	Total counted neurons	c-Fos positive neurons	Mean ± sem %
PV	597	209	35.82 ± 6.53*	465	58	12.36 ± 1.87
NOS	288	11	3.81 ± 2.26	267	9	3.35 ± 2.51
ChAT	721	1	0.14 ± 0.14	640	1	0.16 ± 0.16

Data are presented as neuron numbers and mean ± sem. Quantitative analysis within the nAcc mShell (bregma +1.70 to +0.86 mm) was conducted to determine the number of PV, NOS, or ChAT neurons, and the number of these neurons coexpressing c-Fos. After photostimulation of the VTA VGluT2-inputs, the number of PV neurons within the nAcc mShell coexpressing c-Fos in VGluT2-ChR2-eYFP mice (35.82 ± 6.53%) is significantly more than those in VGluT2-eYFP mice (12.36 ± 1.87%, t_{15}=4.625, *P = 0.0003, Student t-test). Sample size: 73 sections from VGluT2-ChR2-eYFP mice (n = 9) and 65 sections from VGluT2-eYFP mice (n = 8).

Supplementary Table 2. Proportion of c-Fos neurons expressing either D1R mRNA or D2R mRNA in the nAcc mShell of VGluT2-ChR2-eYFP or VGluT2-eYFP mice after photostimulation of the VTA VGluT2-inputs.

	VGluT2-ChR2-eYFP			VGluT2-eYFP		
	Total c-Fos neurons	c-Fos neurons with D1R or D2R mRNA	Mean ± sem %	Total c-Fos neurons	c-Fos neurons with D1R or D2R mRNA	Mean ± sem %
D1R-cells	598	71	12.70 ± 3.19	480	78	18.37 ± 5.89
D2R-cells	262	33	12.22 ± 6.37	360	50	13.8 ± 1.17
Total counted cells	860	104	12.46 ± 3.30	849	128	16.10 ± 2.91

Data are presented as neuron numbers and mean ± sem. Immunodetection of c-Fos was combined with *in situ* hybridization to detect transcripts encoding D1 dopamine receptor (D1R) or D2 dopamine receptor (D2R). Quantitative analysis within the nAcc mShell (bregma +1.70 to +0.86 mm) was conducted to determine the number of c-Fos positive neurons coexpressing either D1R mRNA or D2R mRNA. There is no significant difference of the percentage of total population c-Fos between the VGluT2-ChR2-eYFP mice (12.46 ± 3.30%) and VGluT2-eYFP control mice (16.10 ± 2.91%, t_{14}=0.826, P = 0.42, Student t-test). Sample size: 29 sections for D1R mRNA detection and 24 for D2R mRNA detection from VGluT2-ChR2-eYFP mice (n = 4), and 28 sections for D1R mRNA detection and 29 for D2R mRNA detection from VGluT2-eYFP mice (n = 4).